



SEQUENCE LISTING

<110> Gordon-Kamm, William J.
Lowe, Keith S.
Larkins, Brian A.
Dilkes, Brian R.
Sun, Yuejin

<120> Cell Cycle Nucleic Acids, Polypeptides and Uses Thereof

<130> 1146

<140> 09/993,808

<141> 2001-11-06

<150> 60/246,349

<151> 2000-11-07

<160> 6

<170> PatentIn version 3.1

<210> 1

<211> 1372

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (134)..(904)

<223>

<400> 1
cccacgcgtc cggacgcaag cggctgcagg cagcagcgcc gcgcaggcgt tgtggcctgt 60
gggagaggaa aaagagaaag aggaaccggc caagacaagc aagcgagagg ccagggccgc 120
ggcgttgctg cag atg ggg aag tac atg cgc aag tgc agg ggc gcc gca 169
Met Gly Lys Tyr Met Arg Lys Cys Arg Gly Ala Ala
1 5 10
ggc gcg gag gtc gcc gcc gtc gag gtt acg cag gtc gtc ggc gtc cgg 217
Gly Ala Glu Val Ala Ala Val Glu Val Thr Gln Val Val Gly Val Arg
15 20 25
acg agg tcc agg tcc gcg gcg gcg acc ggc ggt gtc gcg aag gtc gcc 265
Thr Arg Ser Arg Ser Ala Ala Ala Thr Gly Gly Val Ala Lys Val Ala
30 35 40
ccg agg agg aag agg gcg ccg gcg ggg gag cct gct gcc gcc gtg agc 313
Pro Arg Arg Lys Arg Ala Pro Ala Gly Glu Pro Ala Ala Ala Val Ser
45 50 55 60
gct ggt ggg gac ggc gga agc tgc tac atc cac ctg cgt agc cgc atg 361
Ala Gly Gly Asp Gly Gly Ser Cys Tyr Ile His Leu Arg Ser Arg Met
65 70 75

ctg ttc atg gca ccg cct cag ccg cag ccg tcg gtt gac tcg gtt ccg Leu Phe Met Ala Pro Pro Gln Pro Gln Pro Ser Val Asp Ser Val Pro	409
80 85 90	
acc ccg gtg gag gct gct gat ggc gct gca gga cag cag ggc gcg gcg Thr Pro Val Glu Ala Ala Asp Gly Ala Ala Gly Gln Gln Gly Ala Ala	457
95 100 105	
ctc gcg gcc ggg ctc tcg cgt tgc tcc agc acg gcg tcg tcg gtg aac Leu Ala Ala Gly Leu Ser Arg Cys Ser Ser Thr Ala Ser Ser Val Asn	505
110 115 120	
ttg ggc ttg ggg ggt cag cgc ggg agc cac acc tgc cgc tcc tac gac Leu Gly Leu Gly Gly Gln Arg Gly Ser His Thr Cys Arg Ser Tyr Asp	553
125 130 135 140	
gct gca gag gct ggc ggg gat cac gtc ctg gtg gat gtc tcg gcg gcg Ala Ala Glu Ala Gly Gly Asp His Val Leu Val Asp Val Ser Ala Ala	601
145 150 155	
agc aac tcc ggg agc ggc cca gac cgc gag agg cga gag acg acg cca Ser Asn Ser Gly Ser Gly Pro Asp Arg Glu Arg Arg Glu Thr Thr Pro	649
160 165 170	
tcg agc cgg gcg cac ggc gag ctc agc gat ctg gag tcg gat ctg gcg Ser Ser Arg Ala His Gly Glu Leu Ser Asp Leu Glu Ser Asp Leu Ala	697
175 180 185	
ggg cac aag act ggc ccg tcg cta ccg gcg gca acg ccg gct gcg gag Gly His Lys Thr Gly Pro Ser Leu Pro Ala Ala Thr Pro Ala Ala Glu	745
190 195 200	
ctg atc gtg ccg cca gca cac gag atc cag gag ttc ttc gcc gcc gcc Leu Ile Val Pro Pro Ala His Glu Ile Gln Glu Phe Phe Ala Ala Ala	793
205 210 215 220	
gag gcg gcc cag gcc aag cgc ttt gct tcc aag tac aac ttc gac ttc Glu Ala Ala Gln Ala Lys Arg Phe Ala Ser Lys Tyr Asn Phe Asp Phe	841
225 230 235	
gtc cgc ggc gtg ccc ctc gac gcc ggc ggc cgg ttc gag tgg gcg ccg Val Arg Gly Val Pro Leu Asp Ala Gly Gly Arg Phe Glu Trp Ala Pro	889
240 245 250	
gtg gtc agc atc tga agcgagcgtg cgtccggtgc aagggtgaagc tagaaagaga Val Val Ser Ile	944
255	
aaagatgccc cccccccccc cccccaacaa acataacgga gaagagaaaa accaaacaat	1004
taagcagctt tatatagcct aagctaacca ccaccattca tctcgtccaa atgcatgcct	1064
tgctttttctc tggagctagc aggagcgtag ttattattta gtactacttt acttattcag	1124
aggttatctt gaccccgata gatcaatccg cttactgtgt aatttctctc atgcatctct	1184
tagatggagt ttaatcgtct taatttatta ctgtacagca gcttgsttgg cttgcaaaga	1244

aagatctggt ttgtctcaaa aaaaaaaaaa aaaaaaaaaa aaaaaggcg gccgctctag 1304
 aggatccaag cttacgtacg cgtgcatgcg acgtcatagc tcttctatag tgtcacctaa 1364
 attcattc 1372

<210> 2
 <211> 256
 <212> PRT
 <213> Zea mays

<400> 2

Met Gly Lys Tyr Met Arg Lys Cys Arg Gly Ala Ala Gly Ala Glu Val
 1 5 10 15

Ala Ala Val Glu Val Thr Gln Val Val Gly Val Arg Thr Arg Ser Arg
 20 25 30

Ser Ala Ala Ala Thr Gly Gly Val Ala Lys Val Ala Pro Arg Arg Lys
 35 40 45

Arg Ala Pro Ala Gly Glu Pro Ala Ala Ala Val Ser Ala Gly Gly Asp
 50 55 60

Gly Gly Ser Cys Tyr Ile His Leu Arg Ser Arg Met Leu Phe Met Ala
 65 70 75 80

Pro Pro Gln Pro Gln Pro Ser Val Asp Ser Val Pro Thr Pro Val Glu
 85 90 95

Ala Ala Asp Gly Ala Ala Gly Gln Gln Gly Ala Ala Leu Ala Ala Gly
 100 105 110

Leu Ser Arg Cys Ser Ser Thr Ala Ser Ser Val Asn Leu Gly Leu Gly
 115 120 125

Gly Gln Arg Gly Ser His Thr Cys Arg Ser Tyr Asp Ala Ala Glu Ala
 130 135 140

Gly Gly Asp His Val Leu Val Asp Val Ser Ala Ala Ser Asn Ser Gly
 145 150 155 160

Ser Gly Pro Asp Arg Glu Arg Arg Glu Thr Thr Pro Ser Ser Arg Ala
 165 170 175

His Gly Glu Leu Ser Asp Leu Glu Ser Asp Leu Ala Gly His Lys Thr
180 185 190

Gly Pro Ser Leu Pro Ala Ala Thr Pro Ala Ala Glu Leu Ile Val Pro
195 200 205

Pro Ala His Glu Ile Gln Glu Phe Phe Ala Ala Ala Glu Ala Ala Gln
210 215 220

Ala Lys Arg Phe Ala Ser Lys Tyr Asn Phe Asp Phe Val Arg Gly Val
225 230 235 240

Pro Leu Asp Ala Gly Gly Arg Phe Glu Trp Ala Pro Val Val Ser Ile
245 250 255

<210> 3
<211> 1089
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (154)..(726)
<223>

<400> 3
cccacgcgtc cgccctcctg tgtacaccac tcccgcgccg cctaccattt tatccccgcc 60
tctcctggcc tctgccgcc cgtcgcacag aatcgcttgg tgcaccctgc gagggcctcc 120
tcgaaaccct agcttgccca gccccctccg gcc atg ggc aag tac atg cgc aag 174
Met Gly Lys Tyr Met Arg Lys
1 5
gcc aag gct tcc agc gag gtt gtc atc atg gat gtc gcc gcc gct ccg 222
Ala Lys Ala Ser Ser Glu Val Val Ile Met Asp Val Ala Ala Ala Pro
10 15 20
ctc gga gtc cgc acc cga gcg cgc gcc ctc gcg ctg cag cgt ctg cag 270
Leu Gly Val Arg Thr Arg Ala Arg Ala Leu Ala Leu Gln Arg Leu Gln
25 30 35
gag cag cag acg cag tgg gag gaa ggt gct ggc ggc gag tac ctg gag 318
Glu Gln Gln Thr Gln Trp Glu Glu Gly Ala Gly Gly Glu Tyr Leu Glu
40 45 50 55
cta agg aac cgg agg ctc gag aag ctg ccg ccg ccg ccg gcg acc acg 366
Leu Arg Asn Arg Arg Leu Glu Lys Leu Pro Pro Pro Pro Ala Thr Thr
60 65 70
agg agg tcg ggc ggg agg aaa gcg gca gcc gag gcc gcc gca act aag 414
Arg Arg Ser Gly Gly Arg Lys Ala Ala Ala Glu Ala Ala Ala Thr Lys

Leu Ala Leu Gln Arg Leu Gln Glu Gln Gln Thr Gln Trp Glu Glu Gly
 35 40 45

Ala Gly Gly Glu Tyr Leu Glu Leu Arg Asn Arg Arg Leu Glu Lys Leu
 50 55 60

Pro Pro Pro Pro Ala Thr Thr Arg Arg Ser Gly Gly Arg Lys Ala Ala
 65 70 75 80

Ala Glu Ala Ala Ala Thr Lys Glu Ala Glu Ala Ser Tyr Gly Glu Asn
 85 90 95

Met Leu Glu Leu Glu Ala Met Glu Arg Ile Thr Arg Glu Thr Thr Pro
 100 105 110

Cys Ser Leu Ile Asn Thr Gln Met Thr Ser Thr Pro Gly Ser Thr Arg
 115 120 125

Ser Ser His Ser Cys His Arg Arg Val Asn Ala Pro Pro Val His Ala
 130 135 140

Val Pro Ser Ser Arg Glu Met Asn Glu Tyr Phe Ala Ala Glu Gln Arg
 145 150 155 160

Arg Gln Gln Gln Asp Phe Ile Asp Lys Tyr Asn Phe Asp Pro Ala Asn
 165 170 175

Asp Cys Pro Leu Pro Gly Arg Phe Glu Trp Val Lys Leu Asp
 180 185 190

<210> 5
 <211> 841
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (159)..(839)
 <223> The 'r' at location 491 stands for g or a.

<400> 5
 cccacgcgtc cgagtagaat ccaaagcgca agcggctgca gcctgcaggc agcgccgcgc 60
 aggcgtggga gtggccgagt gggagtggga gtgaaaaaga ggaaccggcc aagagaagca 120
 agcgagaaga aggcagtgct gcggcggcgt tccgtaag atg ggg aag tac atg cgc 176
 Met Gly Lys Tyr Met Arg

	1	5	
aag cgc agg ggg gcc gcg ggc gag ggg gtg gcc gca gtc gag gtc tcg			224
Lys Arg Arg Gly Ala Ala Gly Glu Gly Val Ala Ala Val Glu Val Ser			
10 15 20			
cag gtc gtc ggc gtc cgg acg agg tcc agg tcc gcg gcg gcg acc ggc			272
Gln Val Val Gly Val Arg Thr Arg Ser Arg Ser Ala Ala Ala Thr Gly			
25 30 35			
ggc ggt gtc gcg aag gtc gct ccg ccg agg agg aag aag gcg ctg ctg			320
Gly Gly Val Ala Lys Val Ala Pro Pro Arg Arg Lys Lys Ala Leu Leu			
40 45 50			
ccc gcc gcg aac gtg acg acg tcg ggg gag cct ggt gcc gtg ggc gct			368
Pro Ala Ala Asn Val Thr Thr Ser Gly Glu Pro Gly Ala Val Gly Ala			
55 60 65 70			
ggt ggt ggg gac ggc gga agc tgc tgc tac atc cac ctg cgg agc cgc			416
Gly Gly Gly Asp Gly Gly Ser Cys Cys Tyr Ile His Leu Arg Ser Arg			
75 80 85			
atg ctg ttc atg gca gca cct cag cag caa ccg tcg gcg gct ctg acg			464
Met Leu Phe Met Ala Ala Pro Gln Gln Gln Pro Ser Ala Ala Leu Thr			
90 95 100			
ccg gtg gag gct gct ggt gcg gca car caa ggc ggg gtg gtg gcg ctc			512
Pro Val Glu Ala Ala Gly Ala Ala Xaa Gln Gly Gly Val Val Ala Leu			
105 110 115			
gcg gct ggc ctc tcg cgt tgc tcc agc acg gcg tcg tcg gtg gac gtc			560
Ala Ala Gly Leu Ser Arg Cys Ser Ser Thr Ala Ser Ser Val Asp Val			
120 125 130			
ggg ggc cac gcc tgc cgc tcc gac gct gcg cct gcg gag gtt gac ggg			608
Gly Gly His Ala Cys Arg Ser Asp Ala Ala Pro Ala Glu Val Asp Gly			
135 140 145 150			
gat cac gtc ccg gat gtc gtc acc gcg agc aac tcg ggg agc gtc ccg			656
Asp His Val Pro Asp Val Val Thr Ala Ser Asn Ser Gly Ser Val Pro			
155 160 165			
gac cgc gag agg aga gag acg acg cca tcg tcg agc cgg gcg cac ggc			704
Asp Arg Glu Arg Arg Glu Thr Thr Pro Ser Ser Ser Arg Ala His Gly			
170 175 180			
ggc gag ctc agc gat ctg gag tcg gat ctg gtg ggg cgg cag aag act			752
Gly Glu Leu Ser Asp Leu Glu Ser Asp Leu Val Gly Arg Gln Lys Thr			
185 190 195			
ggc tgc tcg tcg tcg ccg gcg aca aca aca tcg gct gcg gag ctg atc			800
Gly Cys Ser Ser Ser Pro Ala Thr Thr Thr Ser Ala Ala Glu Leu Ile			
200 205 210			
gtg ccg cca gca cag gag atc cag gaa ttc ttc gcg gcc gc			841
Val Pro Pro Ala Gln Glu Ile Gln Glu Phe Phe Ala Ala			
215 220 225			

<210> 6
 <211> 227
 <212> PRT
 <213> Zea mays

<220>
 <221> misc_feature
 <222> (111)..(111)
 <223> The 'Xaa' at location 111 stands for Gln.

<400> 6

Met Gly Lys Tyr Met Arg Lys Arg Arg Gly Ala Ala Gly Glu Gly Val
 1 5 10 15

Ala Ala Val Glu Val Ser Gln Val Val Gly Val Arg Thr Arg Ser Arg
 20 25 30

Ser Ala Ala Ala Thr Gly Gly Gly Val Ala Lys Val Ala Pro Pro Arg
 35 40 45

Arg Lys Lys Ala Leu Leu Pro Ala Ala Asn Val Thr Thr Ser Gly Glu
 50 55 60

Pro Gly Ala Val Gly Ala Gly Gly Gly Asp Gly Gly Ser Cys Cys Tyr
 65 70 75 80

Ile His Leu Arg Ser Arg Met Leu Phe Met Ala Ala Pro Gln Gln Gln
 85 90 95

Pro Ser Ala Ala Leu Thr Pro Val Glu Ala Ala Gly Ala Ala Xaa Gln
 100 105 110

Gly Gly Val Val Ala Leu Ala Ala Gly Leu Ser Arg Cys Ser Ser Thr
 115 120 125

Ala Ser Ser Val Asp Val Gly Gly His Ala Cys Arg Ser Asp Ala Ala
 130 135 140

Pro Ala Glu Val Asp Gly Asp His Val Pro Asp Val Val Thr Ala Ser
 145 150 155 160

Asn Ser Gly Ser Val Pro Asp Arg Glu Arg Arg Glu Thr Thr Pro Ser
 165 170 175

Ser Ser Arg Ala His Gly Gly Glu Leu Ser Asp Leu Glu Ser Asp Leu

180

185

190

Val Gly Arg Gln Lys Thr Gly Cys Ser Ser Ser Pro Ala Thr Thr Thr
195 200 205

Ser Ala Ala Glu Leu Ile Val Pro Pro Ala Gln Glu Ile Gln Glu Phe
210 215 220

Phe Ala Ala
225